



FIG. 1

SP22	MASKRALVILAKGAEEMETVI <u>PVDIMRRAGIKVTVAGLAG</u>	
1	: : : : : : :	40
DJ-1	MASKRALVILAKGAEEMETVI <u>PVDVMRRAGIKVTVAGLAG</u>	
	Peptide 1	
SP22	<u>KDPVQCSR</u> <u>DVVICPDTSLEEAKTQGPYDVVVLPGGNLGAQ</u>	
41	: : : : : : :	80
DJ-1	<u>KDPVQCSR</u> <u>DVVICPDASLEAKKEGPYDVVVLPGGNLGAQ</u>	
SP22	NLSESAV <u>KEILKE</u> QENRKGLIAAI <u>CAGPTALLAHEVGFG</u>	
81	: : : : : : :	120
DJ-1	NLSESAAV <u>KEILKE</u> QENRKGLIAAI <u>CAGPTALLAHEIGCG</u>	
	Peptide 2	
SP22	CKVT <u>SHPLAKD</u> KMMNGSHYSYSERVE <u>KDGLILTSRGPGT</u>	
121	: : : : : : : :	160
DJ-1	SKVT <u>THPLAKD</u> KMMNGGHYTYSERVE <u>KDGLILTSRGPGT</u>	
	Peptide 3	
	Peptide 4	
SP22	SFEFALAIIVEALSGKDMANQVKAPLVLD	
161	: : : : : :	189
DJ-1	SFEFALAIIVEALNGKEVAAQVKAPLVLD	

FIG. 2

1 A gctgtgcagagccgtctggcagggttacccatctttattaatcattag 65
 66 A tagtgtggtcagagacttagcaccattgtctccccaacctggccagacatttcagcagtta 130
 131 A tcggaacagcaacaacagcaacaaaacccaaaattacaatctttaagaatagaaATGgca 195
 B tggcttcgcgtgggtggaggaggcgcggctcaggtctttaagaatagaaATGgca
 C ttqaacctATGttqcactqtqqaqttctccacttacacacqccctatttatggca
 1 M L H C G V L H L H S L F M A 15
 196 tccaaaagagctctggtcacccatccaaaggagcagaggagatggagacagtgattcctgtgga 260
 16 S K R A L V I L A K G A E E M E T V I P V D 37
 261 catcatgcggcgagctgggattaaagtcacccgtgcaggcttggctggaaaggaccccgtgcagt 325
 38 I M R R A G I K V T V A G L A G K D P V O 58
 Peptide 1
 326 gtagccgtatgtatgtatccggataccagtctggaaaggcaaaaacacagggaccatac 390
 59 C S R D V V I C P D T S L E E A K T Q G P Y 80
 391 gatgtgggtgttcttcaggagggaaatctgggtgcacagaacttatctgagtcggcttggtgaa 455
 81 D V V V L P G G N L G A Q N L S E S A L V K 102
 456 ggagatcccaaggagcaggagaacaggaaggccatagctgcacatctgtgcgggtcctacgg 520
 103 E I L K E Q E N R K G L I A A I C A G P T 123
 Peptide 2
 *
 521 ccctgtggctacagaagttaggcttggatgcaaggatcacatcgccaccattggctaaggacaaa 585
 124 A L L A H E V G F G C K V T S H P L A K D K 145
 Peptide 3
 586 atgatgaacggcagtcaactacagctactcagagagccgtgtggagaaggacggccatcctcac 650
 146 M M N G S H Y S Y S E S R V E K D G L I L T 167
 Peptide 4
 651 cagccgtggccctggaccagcttcgagttgcgcgtggccattgtggaggcactcagtggcaagg 715
 168 S R G P G T S F E F A L A I V E A L S G K 188
 716 acatggctaaccaagtgaaggccccgttgcgttcaaagactAGagagcccaagccctggaccct 780
 189 D M A N Q V K A P L V L K D * 202
 781 ggaccccccaggctgagcaggcatttggaaagcccactagagagaccacagccaggtaacctggcat 845
 846 tggaagcccacttagtgttccacagccaggtaacctcaggaactaacgtgtgaagttagccgct 910
 911 gctcaggaatctcgccctggctctgtactattctgagccttgcttagaataaacagttcccca 975
 976 agctc*c*tgacggct* 989

Fig. 3

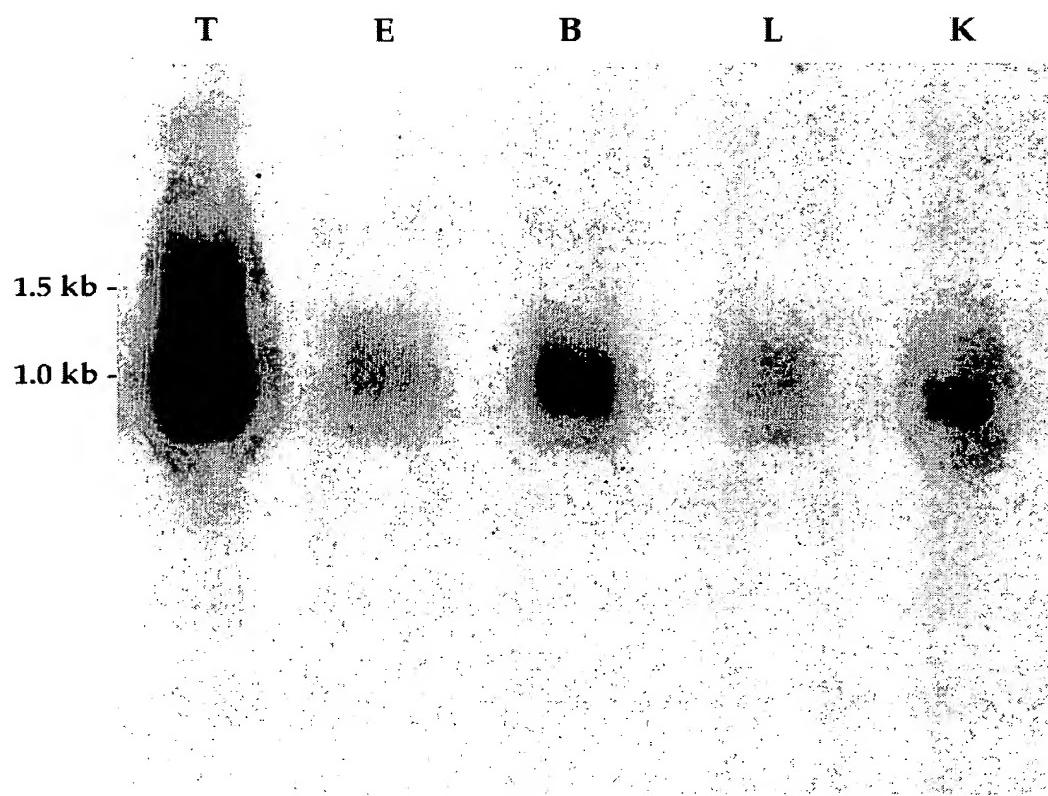


Fig. 4

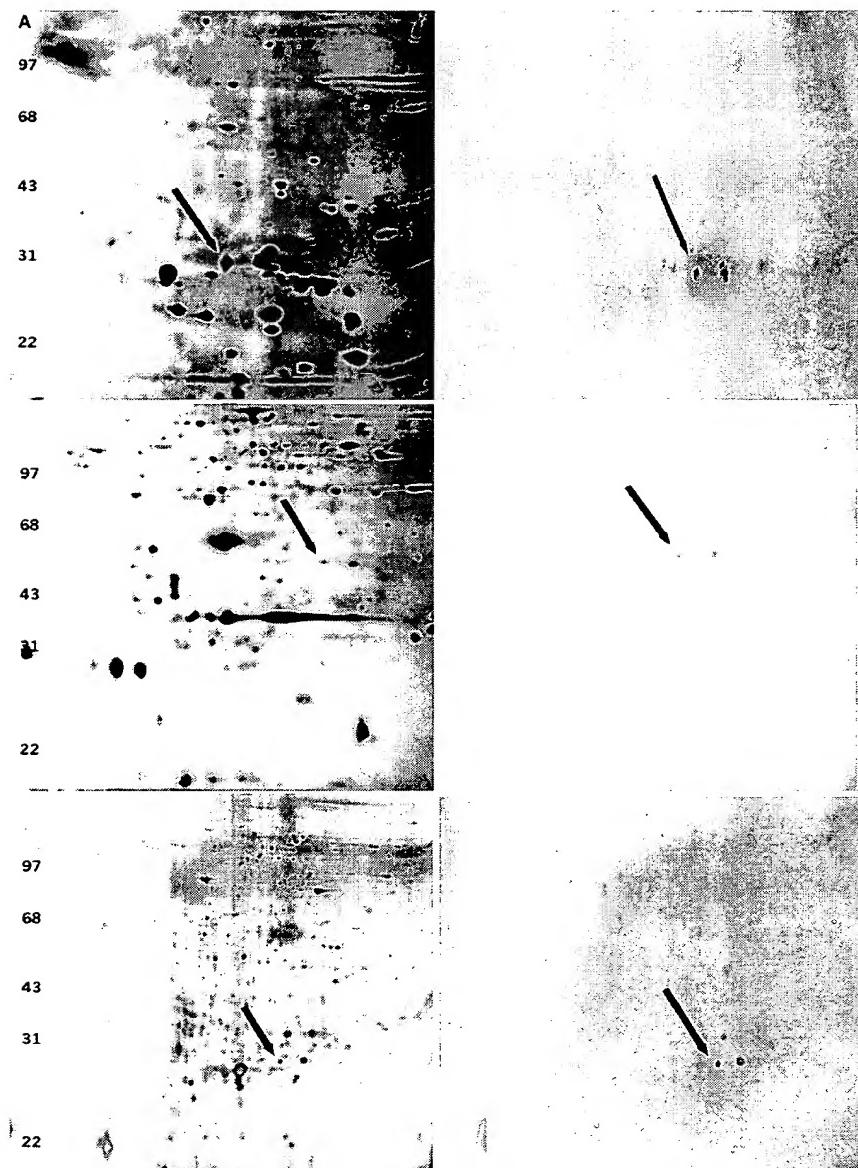


Fig. 5

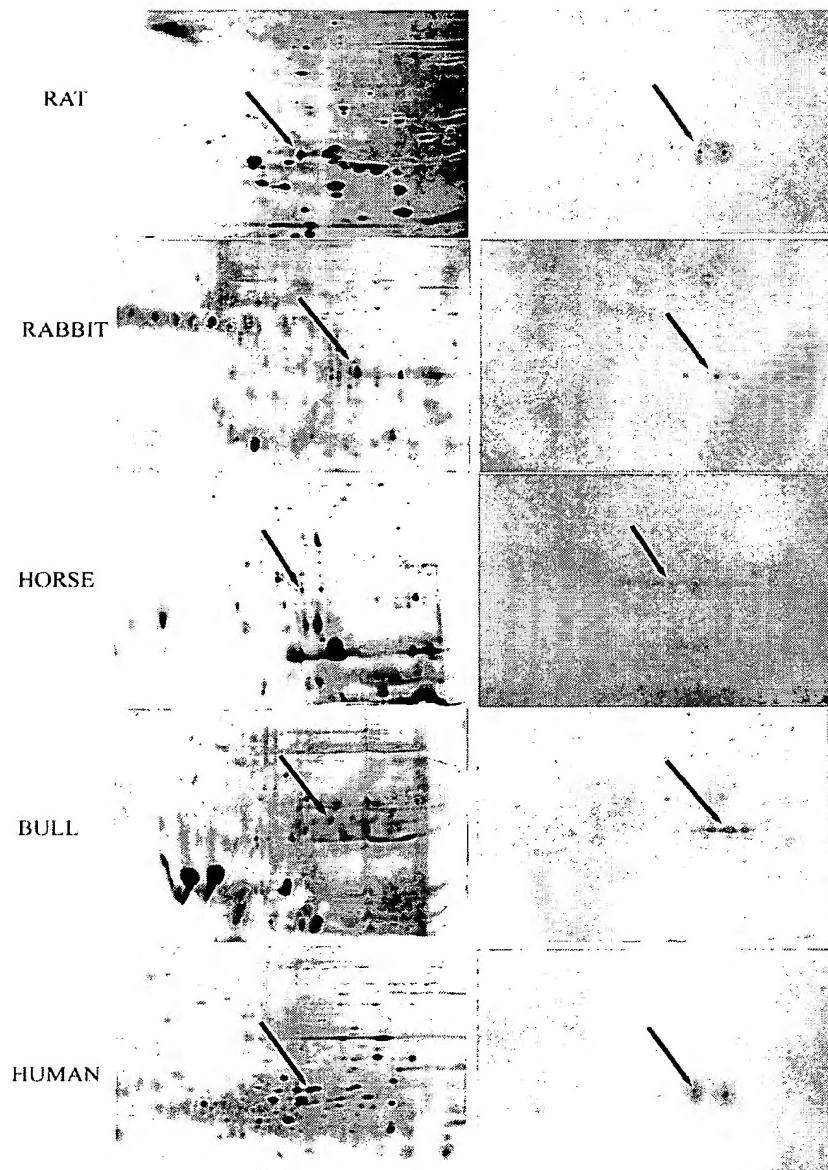
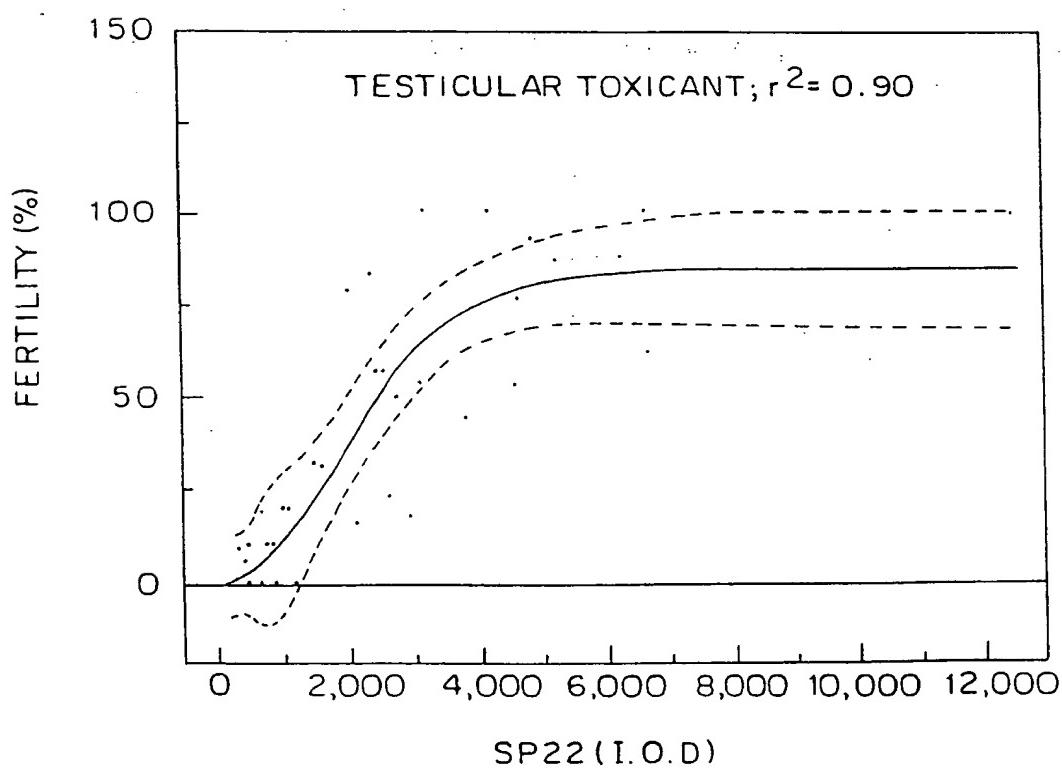
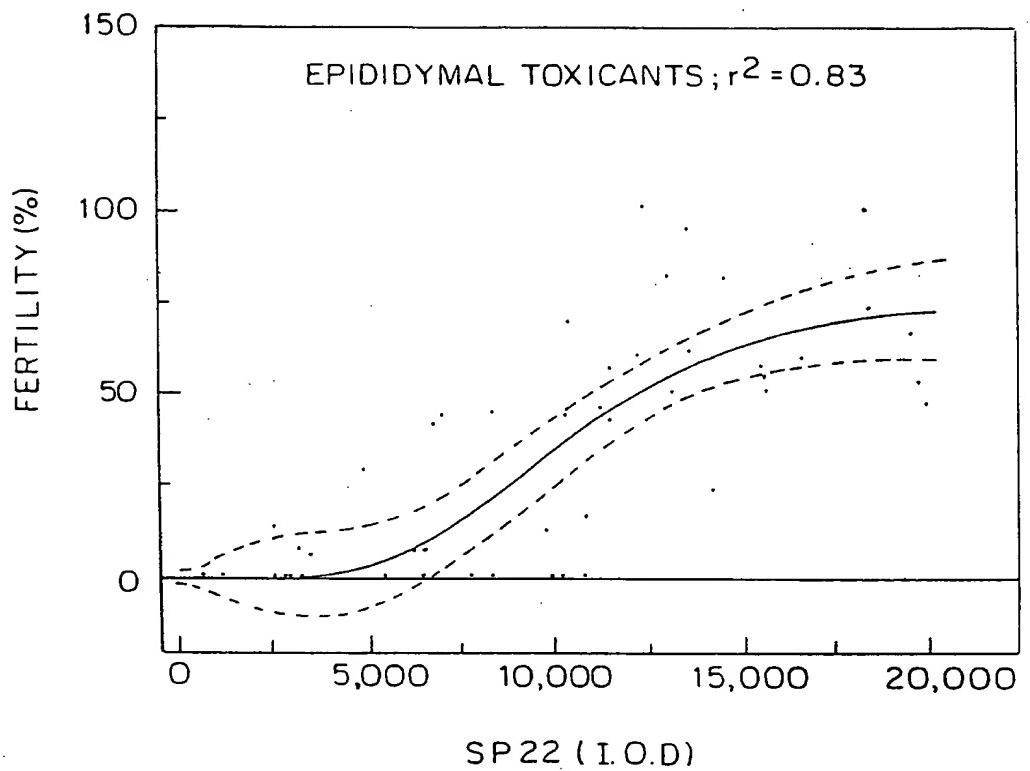


FIG. 6



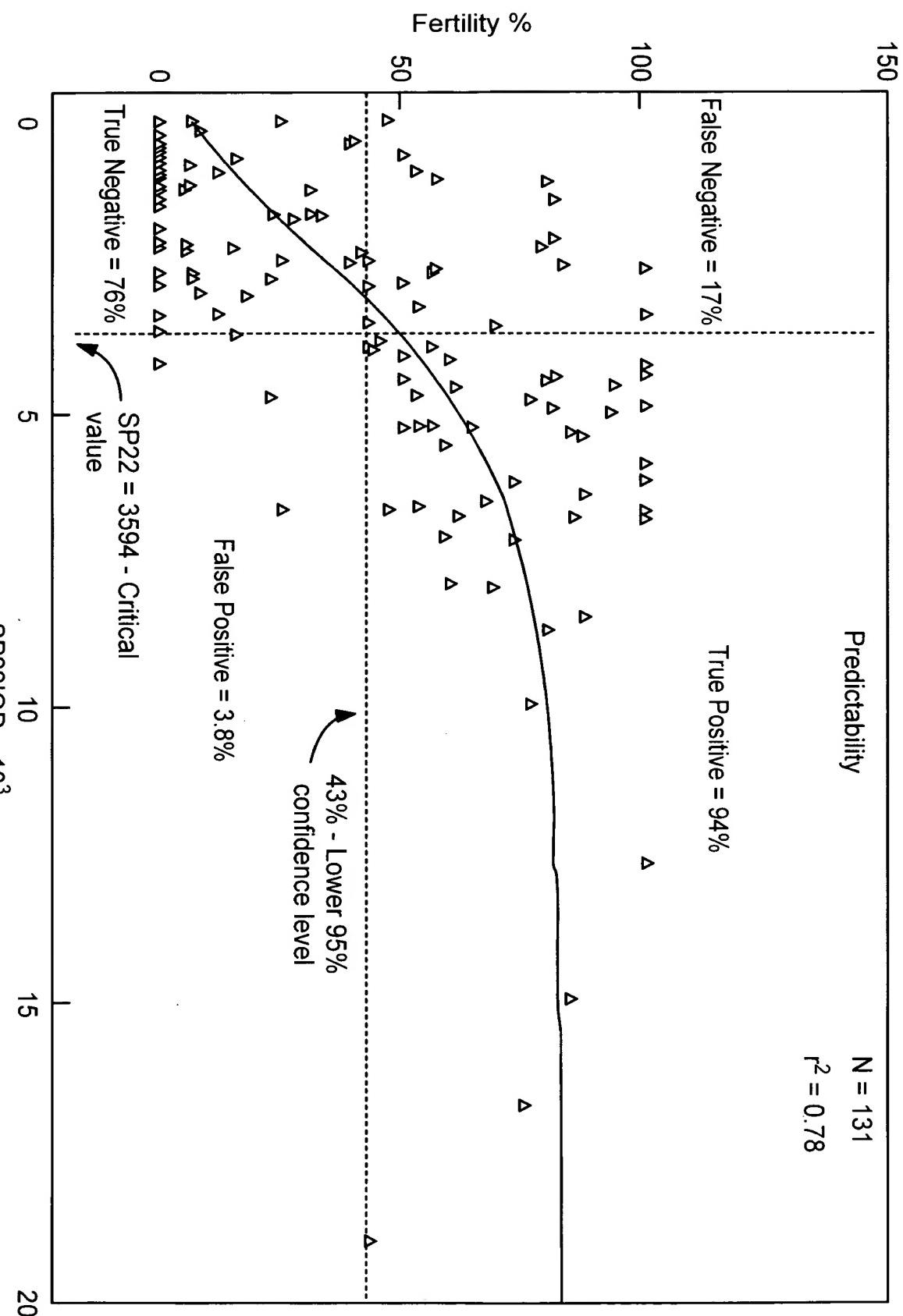


FIG.
7

FIG. 8-1

FIG. 8-2

FIG. 8-3

FIG. 8

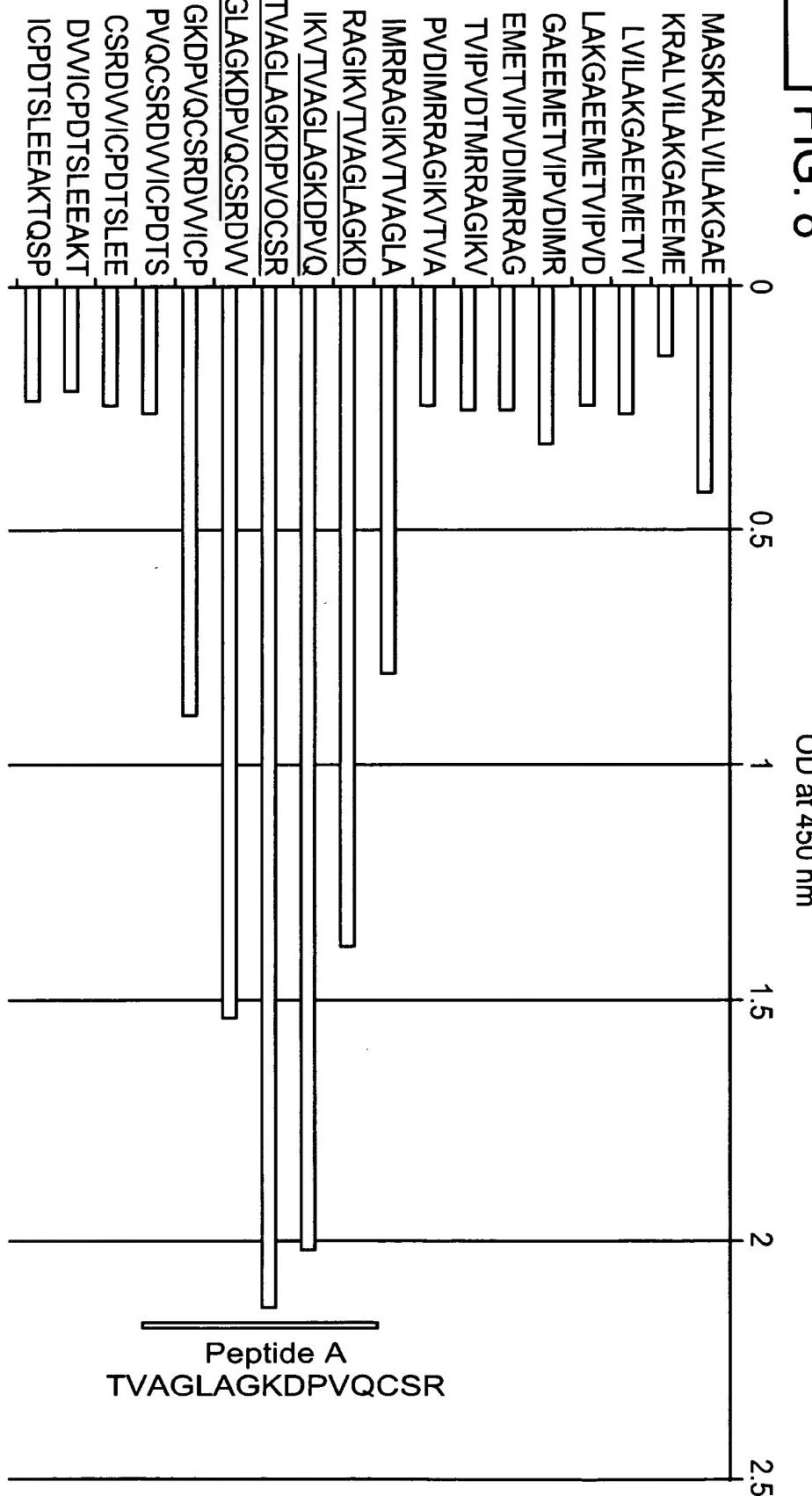


FIG. 8-1

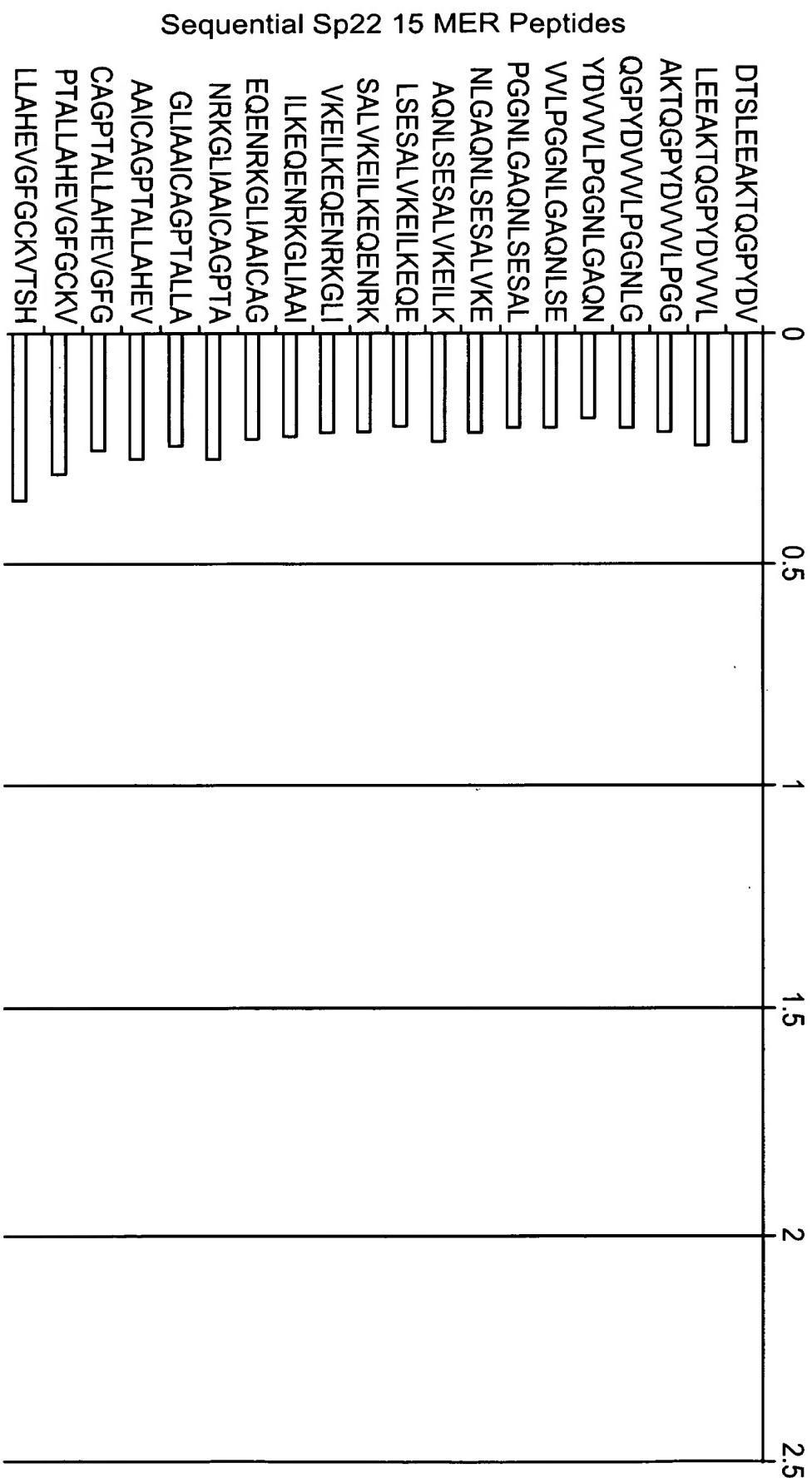


FIG. 8-2

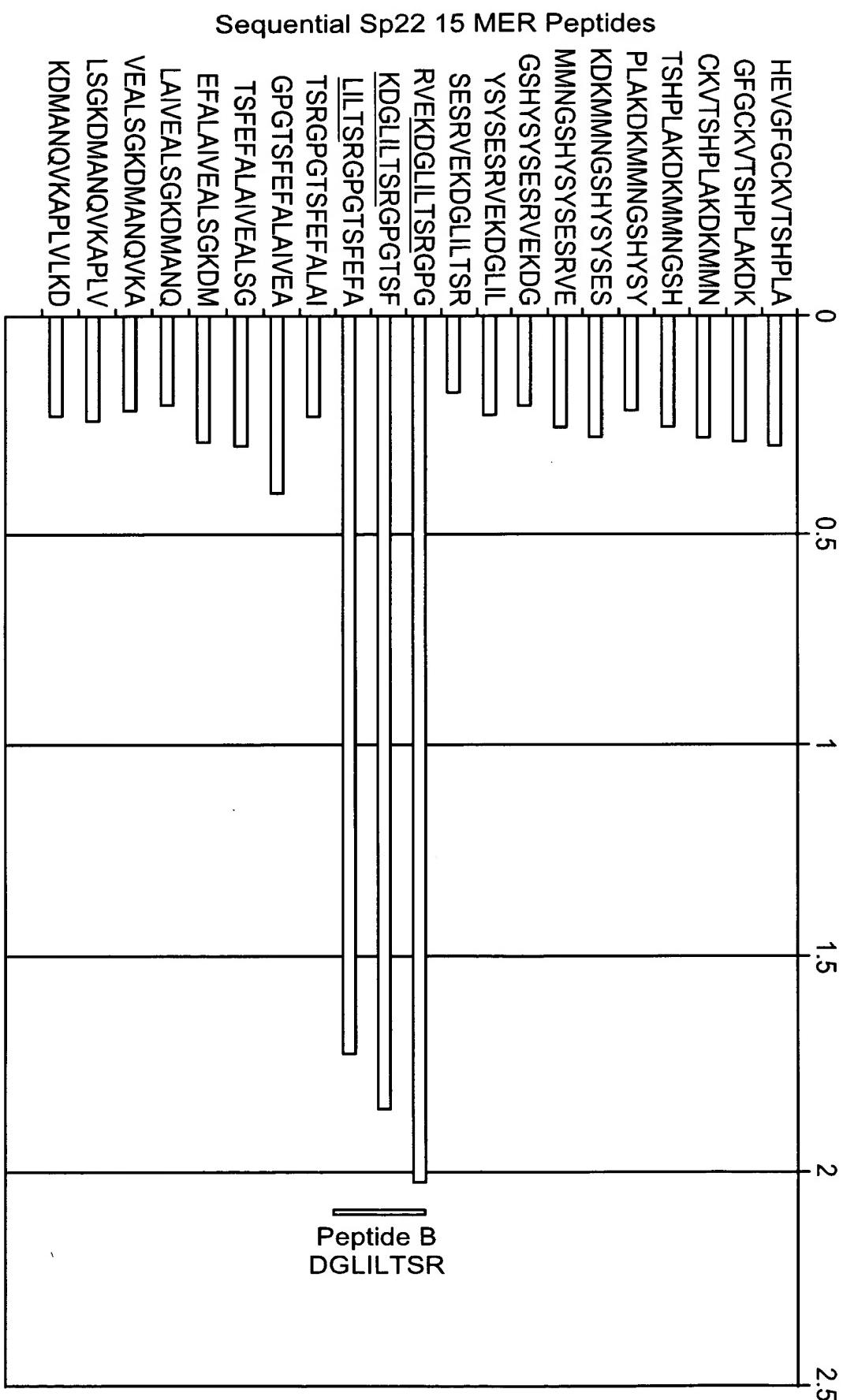


FIG. 8-3

Fig. 9

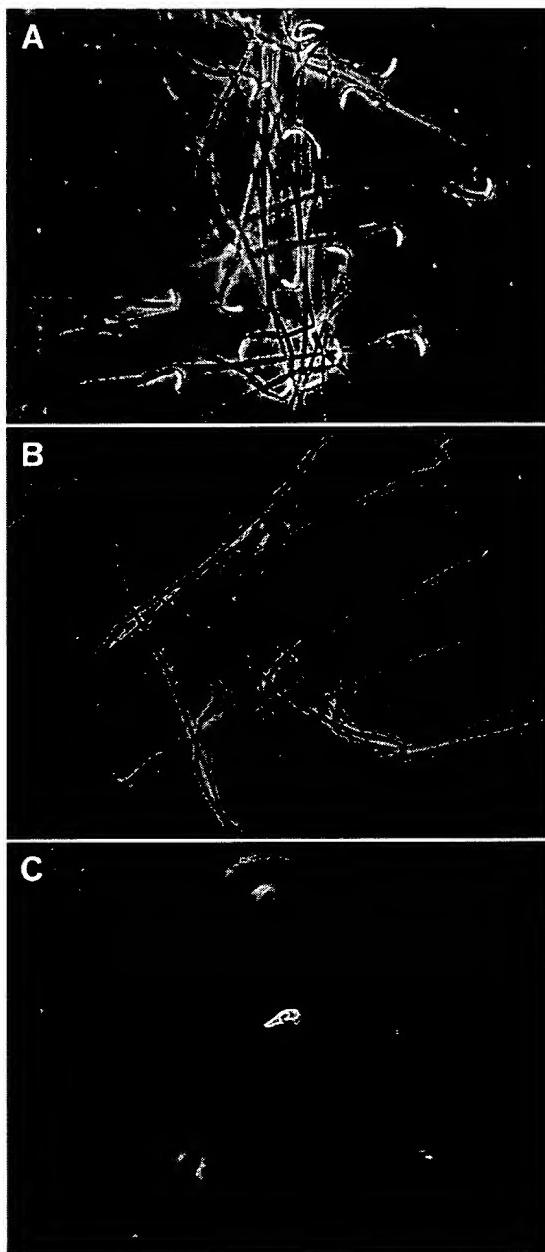


Fig. 10

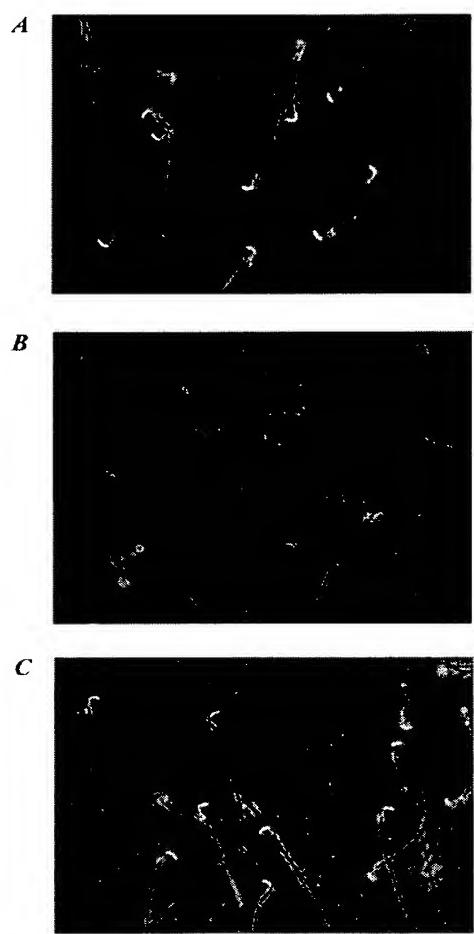
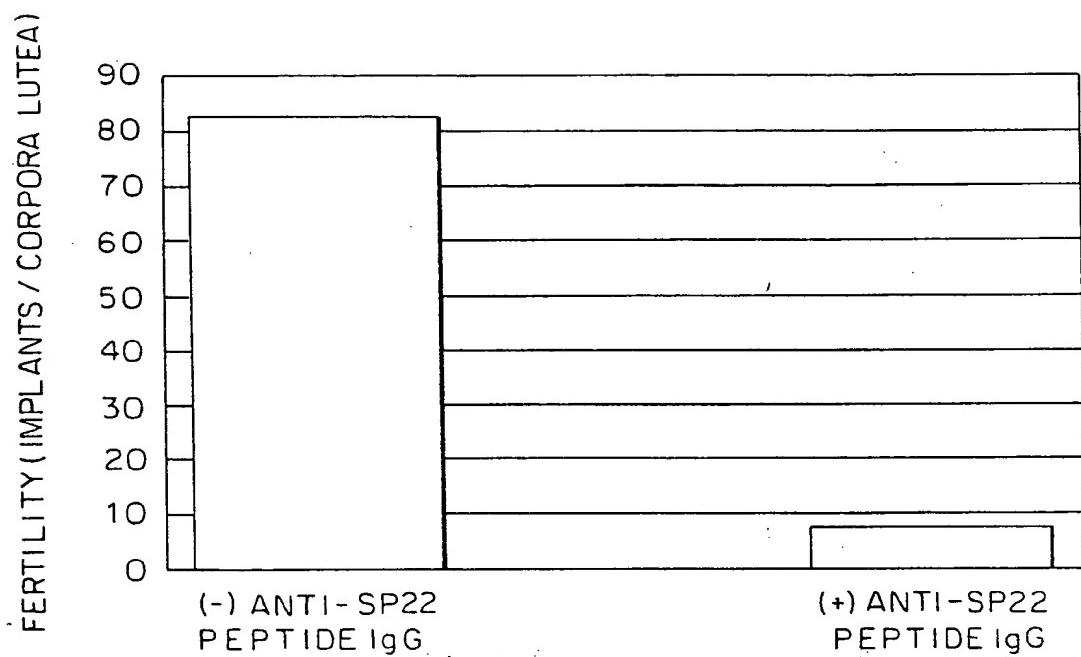


FIG. 11



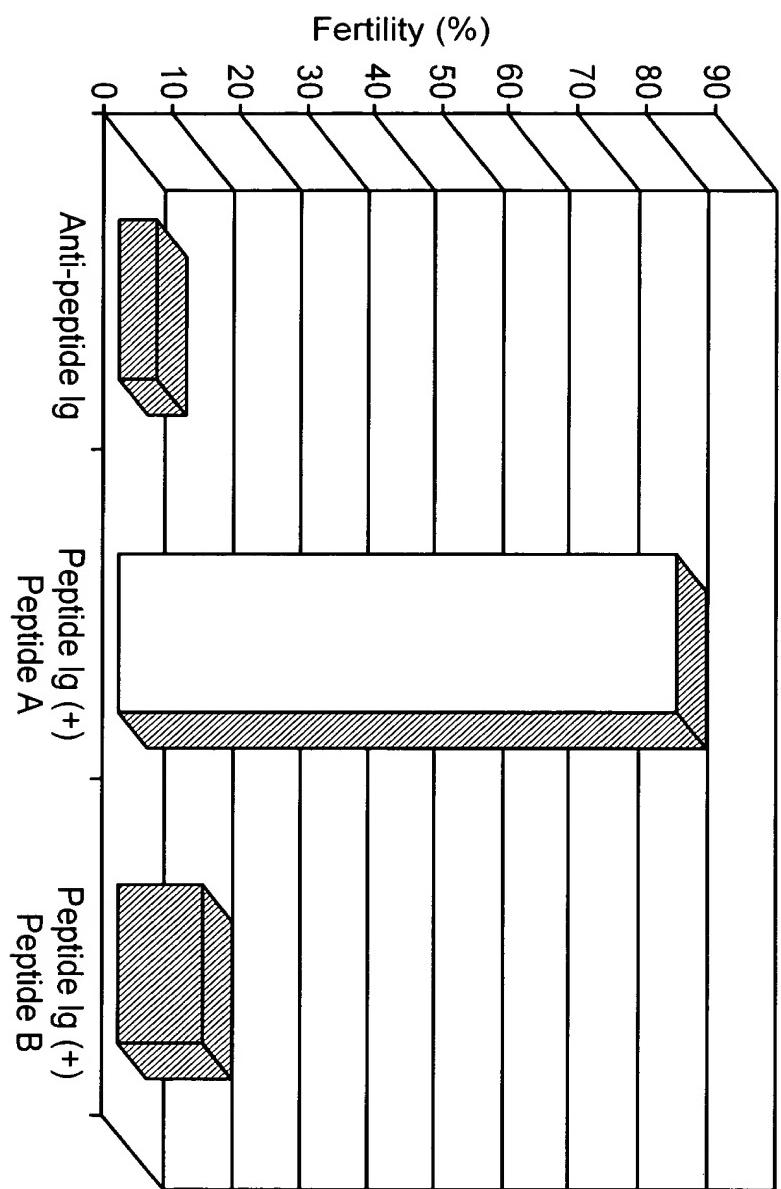


FIG. 12

FIG. 13-1

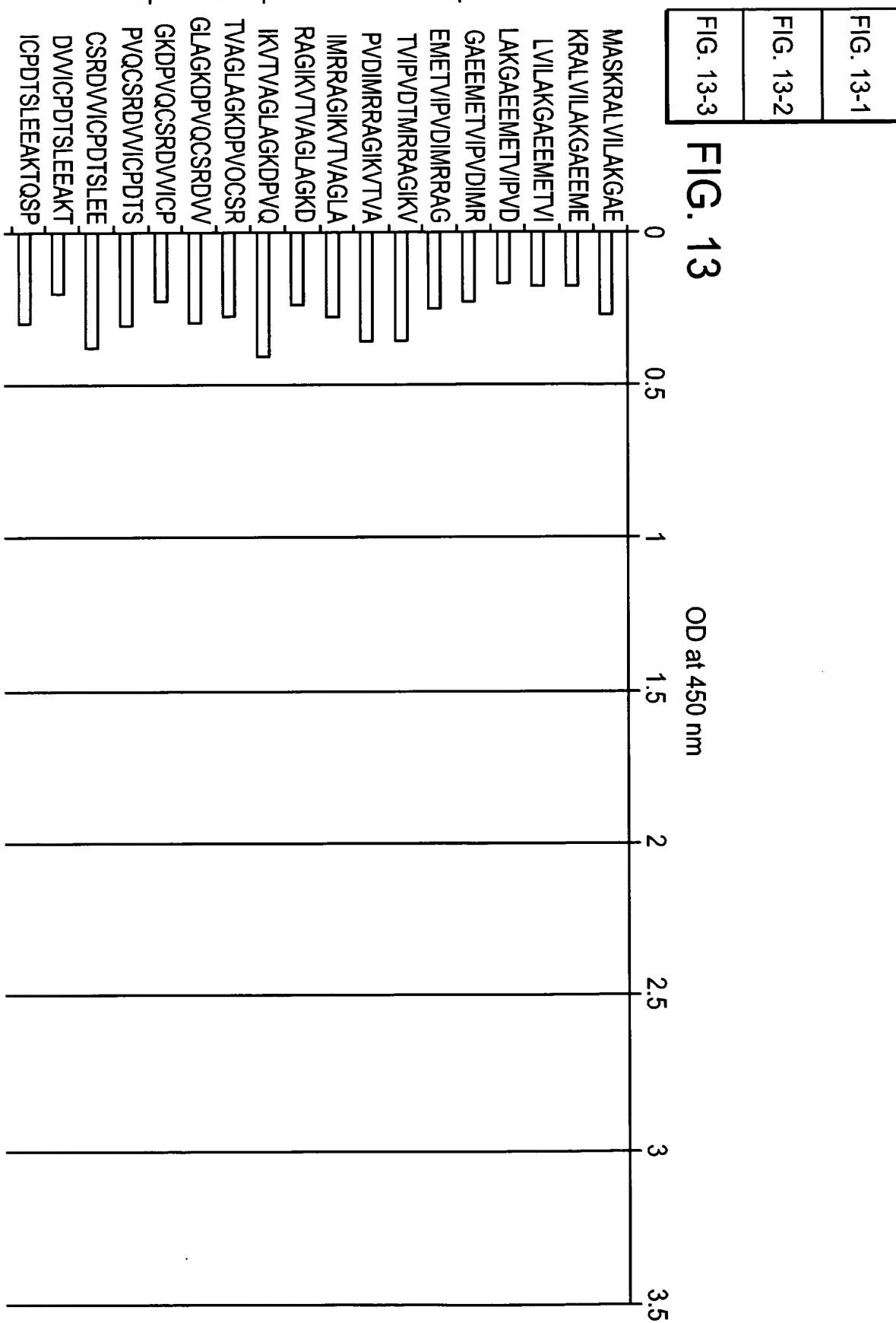
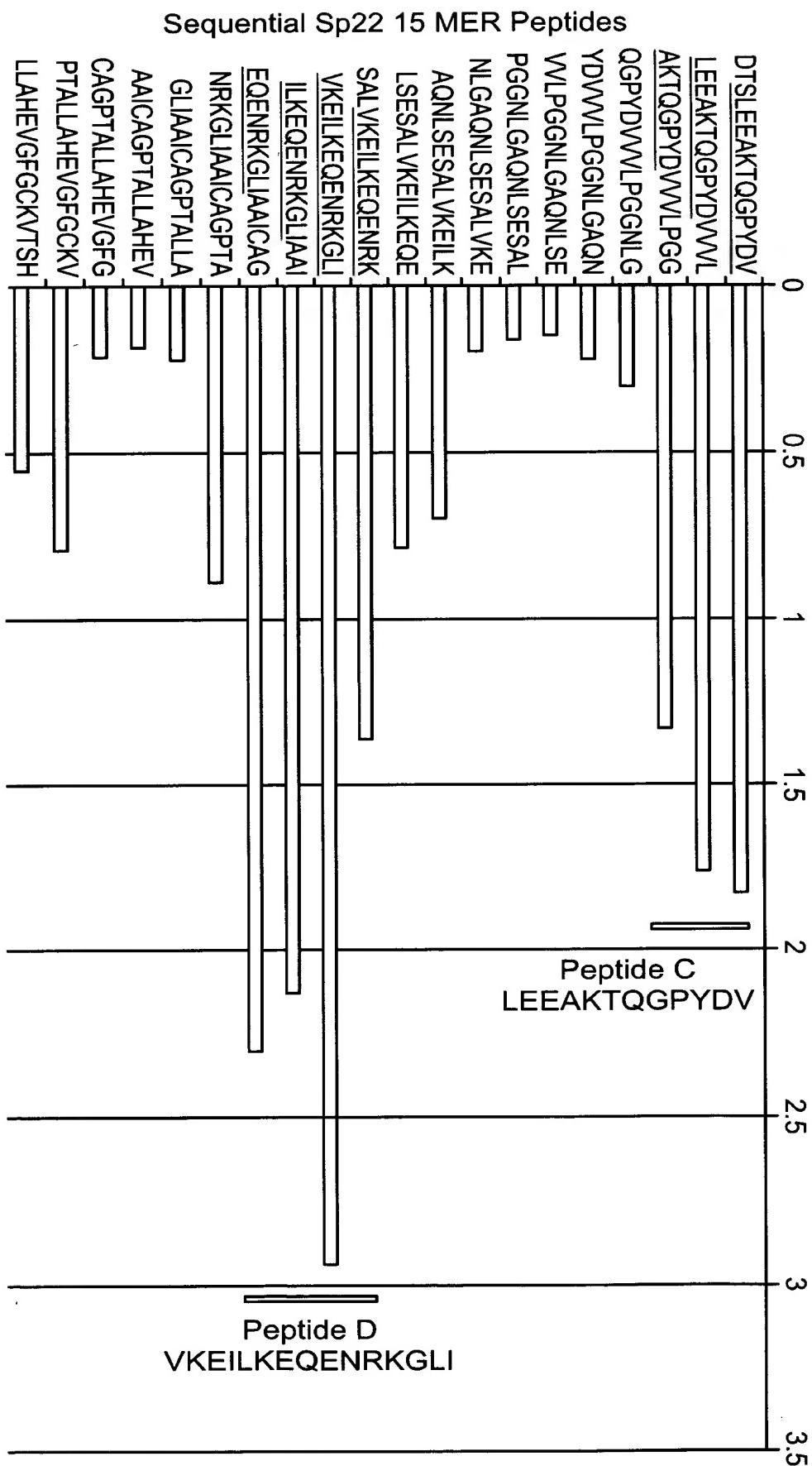


FIG. 13-2



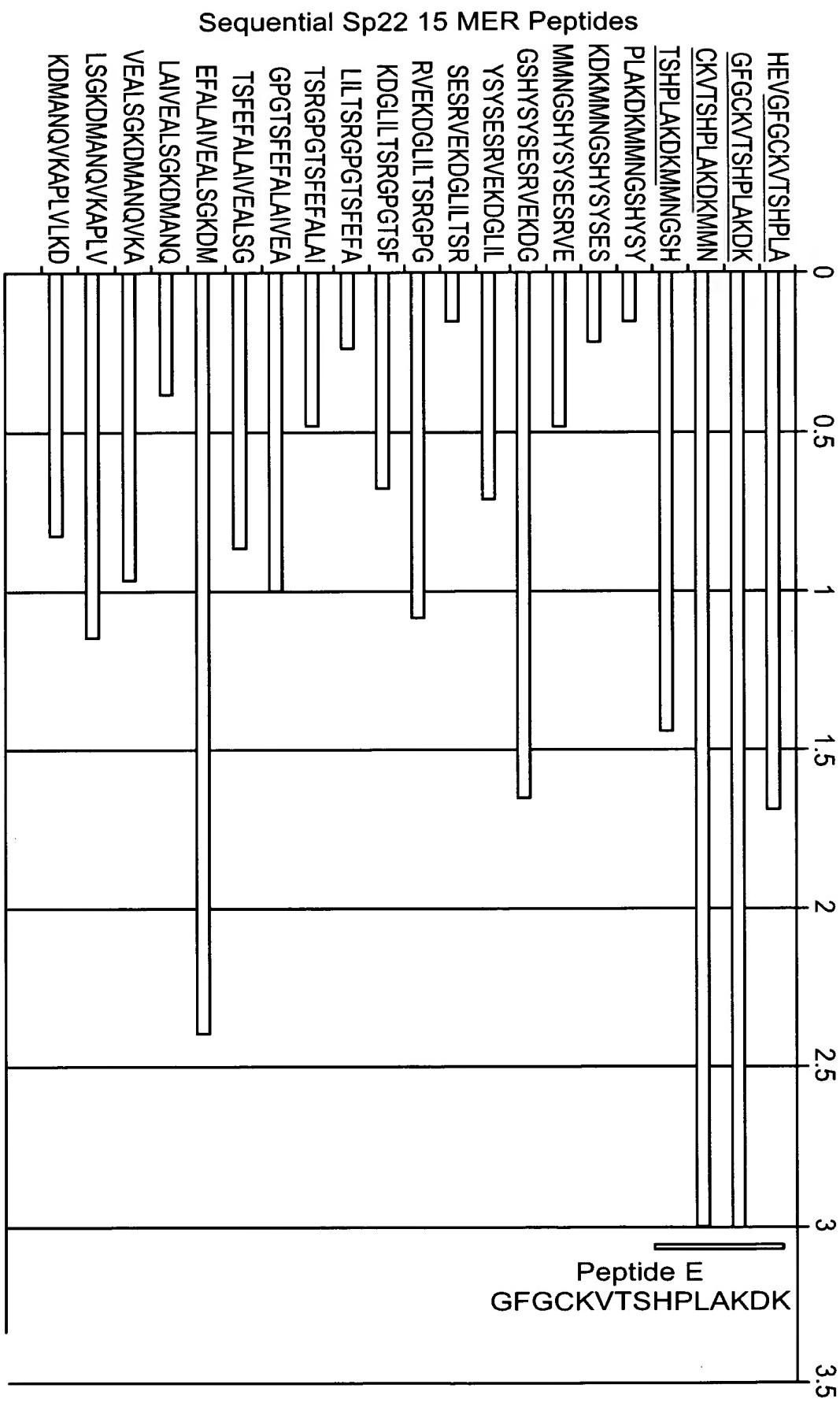


FIG. 13-3

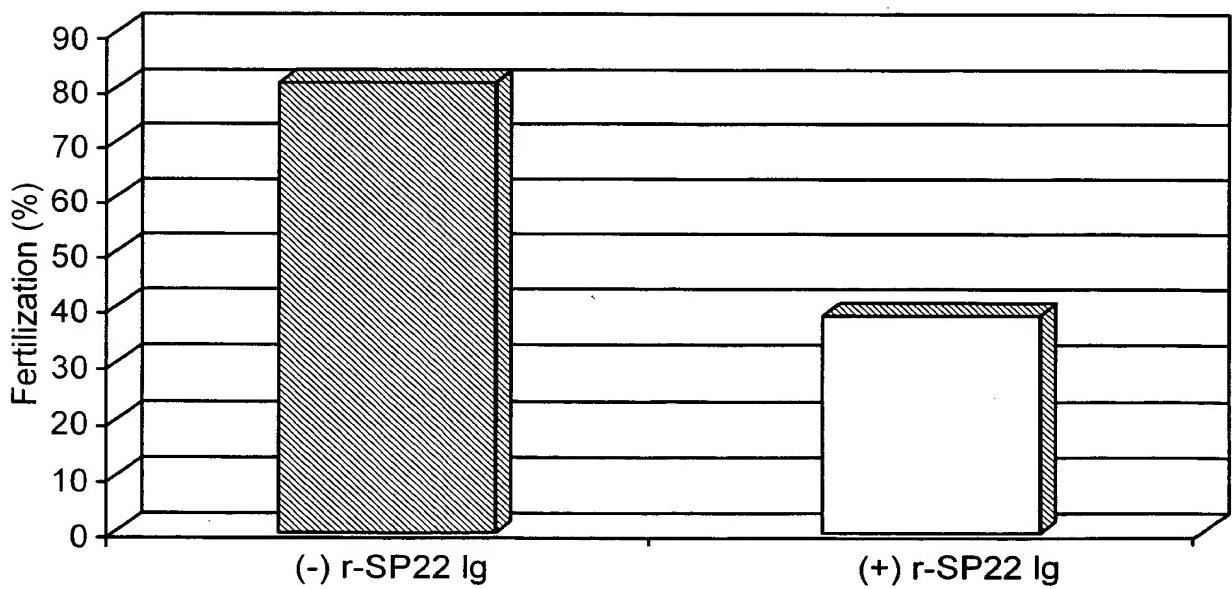
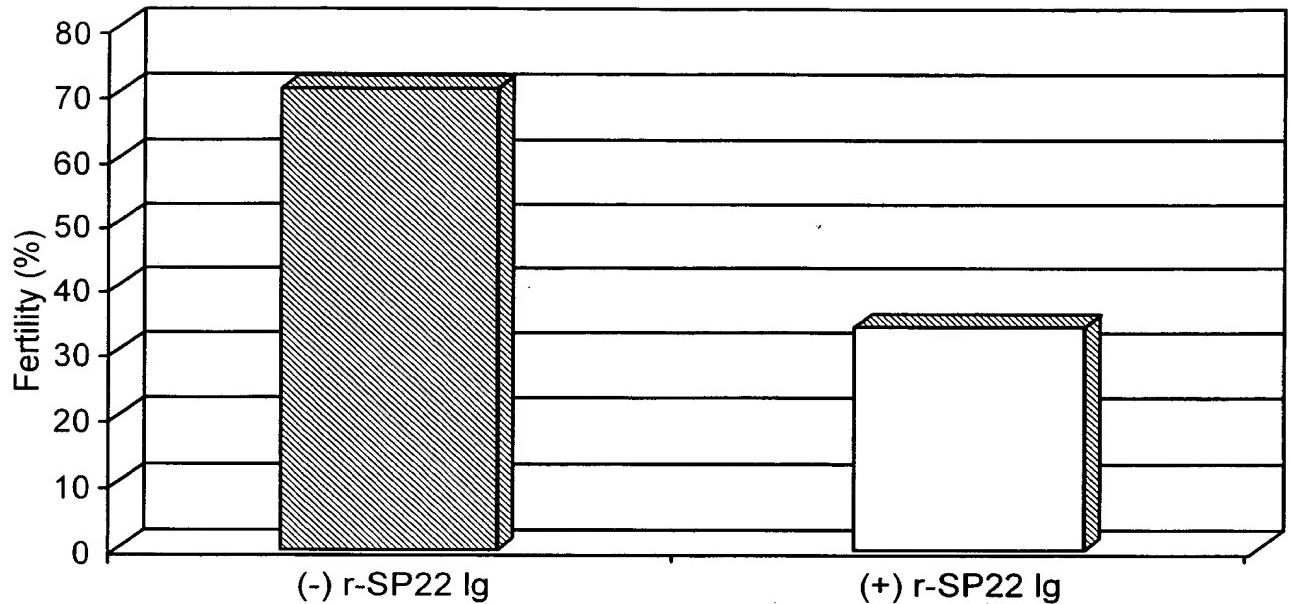


FIG. 14

FIG. 15

1 xxatggcatccaaaagagctctggtcatc 66
 1 X X X X X X X X X X X X M A S K R A L V I 22
 67 ctagccaaaggagcagaggagatggagacagtgattcctgtggacatcatgcggcgagctgggatt 132
 23 L A K G A E E M E T V I P V D I M R R A G I 44
 133 aaagtccaccgttgcaggcttggctggaaaggaccccgtgcagtgtagccgtatgtatgtatgt 198
 45 K V T V A G L A G K D P V Q C S R D V V I C 66
 199 ccggataccagtctggaagaagcaaaaacacagggaccatacgtatgtggttttccaggagga 264
 67 P D T S L E E A K T Q G P Y D V V V L P G G 88
 265 aatctgggtgcacagaacttatctgagtcggcttggtaaggagatcctaaggagcaggagaac 330
 89 N L G A Q N L S E S A L V K E I L K E Q E N 110
 331 aggaagggcctcatagctgccatctgtgcgggtcctacggccctgctggcacgaagttaggctt 396
 111 R K G L I A A I C A G P T A L L A H E V G F 132
 397 ggatgcaagggttacatcgcacccattggctaaggacaaaatgatgaacggcagtcactacagctac 462
 133 G C K V T S H P L A K D K M M N G S H Y S Y 154
 463 tcagagagccgtgtggagaaggacggcctcatcctcaccagccgtggcctggaccagcttcgag 528
 155 S E S R V E K D G L I L T S R G P G T S F E 176
 528 ttgcgcgtggccattgtggaggcactcagtgcaaggacatggctaaccaaagtgaaggccccgctt 594
 177 F A L A I V E A L S G K D M A N Q V K A P L 198
 595 gttctcaaagactagagagcccaagccctggaccctggaccccccagggctgagcaggcatttggaaagc 660
 199 V L K D * 202
 661 ccactagagagaccacagccagtgaacctggcatttggaaaggccactagtggtccacagccagt 726
 727 gaacctcaggaactaacgtgtgaagttagccgcgtcaggaatctcgccctggctctgtactatt 792
 793 ctgagcccttgcgttagataataacagttccccaaagctc 830

FIG. 16

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1      gctgtgcagagccgtctggcagggttacccctaaaggatattccatcttattaatcattag 65
66     tagtgtggtcagagacttagcaccattggtctcccccaacctggtccagacatccagttta 130
131    tcggaacagcaacaacagcaacaaaaccttcaaaattacaagtcttaagaaaatagaaATGgca 195
1                               M A 2
196    tccaaaagagctctggtcatcctagccaaaggagcagaggagatggagacagtgattcctgtgga 260
3       S K R A L V I L A K G A E E M E T V I P V D 24
261    caccatgcggcgagctgggattaaagtaccgttgcaggcttgctggaaaggaccccgtgcagt 325
25       I M R R A G I K V T V A G L A G K D P V Q 45
326    gtagccgtgatgttagtgatttgcggataccagtctggaagaagcaaaaacacagggaccatac 390
46       C S R D V V I C P D T S L E E A K T Q G P Y 67
391    gatgtggttgttcttccaggagggaaatctgggtgcacagaacttatctgagtcggcttggtaa 455
68       D V V V L P G G N L G A Q N L S E S A L V K 89
456    ggagatcctcaaggagcaggagaacaggaaggcctcatagctgccatctgtgcgggtccacgg 520
90       E I L K E Q E N R K G L I A A I C A G P T 110
521    ccctgctggctcacgaagttaggcttggatgcaaggttacatcgcacccattggctaaggacaaa 585
111    A L L A F E V G F G C K V T S H P L A K D K 132
586    atgatgaacggcagtcactacagctactcagagagccgtgtggagaaggacggcctcatcctcac 650
133    M M N G S H Y S Y S E S R V E K D G L I L T 154
651    cagccgtggccctgggaccagcttcgagttgcgtggccattgtggaggcactcagtgccaagg 715
155    S R G P G T S F E F A L A I V E A L S G K 175
716    acatggctaaccaagtgaaggcccccttgcattcaaagacTAGagagcccaagccctggaccct 780
176    D M A N Q V K A P L V L K D 189
781    ggaccccccaggctgagcaggcattggaagcccactagtggtccacagccagtgAACCTGGCAT 845
846    tggaagcccactagtgtgtccacagccagtgAACCTCAGGAACACTAAGCTGTGAAGTAGCCCGCT 910
911    gctcaggaatctcgccctggctctgtactattctgagccttgcttagataaaacagttccccca 975

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